

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA A.  
COHEN, MAURICE  
COLPITTS, TRACEY L.  
FRIEDMAN, PAULA N.  
HAYDEN, MARK  
KLASS, MICHAEL R.  
ROBERTS-RAPP, LISA  
RUSSELL, JOHN C.  
STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE GASTROINTESTINAL  
TRACT

(iii) NUMBER OF SEQUENCES: 51

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Abbott Laboratories  
(B) STREET: 100 Abbott Park Road  
(C) CITY: Abbott Park  
(D) STATE: IL  
(E) COUNTRY: USA  
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/829,754  
(B) FILING DATE: 31-MAR-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Becker, Cheryl L.  
(B) REGISTRATION NUMBER: 35,441  
(C) REFERENCE/DOCKET NUMBER: 6067.US.P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 847/935-1729  
(B) TELEFAX: 847/938-2623  
(C) TELEX:

10840

00049696 032798

84

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| GAAATCACAG | GGAGATGTAC | AGCAATGGGG | CCATTTAAGA  | GTTCTGTGTT | CATCTTGATT | 60  |
| CTTCACCTTC | TAGAAGGGGC | CCTGAGTAAT | TCACCTCATTC | AGCTGAACAA | CAATGGCTAT | 120 |
| GAAGGCATTG | TCGTTGCAAT | CGACCCCAAT | GTGCCAGAAG  | ATGAAACACT | CATTCAACAA | 180 |
| ATAAAGGACA | TGGTGACCCA | GGCATCTCTG | TATCTGTTTG  | AAG        |            | 223 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 158
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 221
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 231
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 251
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| GTTGCAATCG | ACCCCAATGT  | GCCAGAAGAT | GAAACACTCA | TTCAACAAAT | AAAGGACATG | 60  |
| GTGACCCAGG | CATCTCTGTA  | TCTGTTTGAA | GCTACAGGAA | AGCGATTTTA | TTTCAAAAAT | 120 |
| GTTGCCATTT | TGATTCTCTGA | AACATGGAAG | ACAAAGGNTG | ACTATGTGAG | ACCAAAACTT | 180 |
| GAGACCTACA | AAAAATGCTGA | TGTTCTGGTT | GCTGAGTCTA | NTCCTCCAGG | NAATGATGAA | 240 |
| CCCTACACTG | NGCAGATGGG  | CAACTGTGGC | GAG        |            |            | 273 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| AAAATGCTGA | TGTTCTGGTT | GCTGAGTCTA | CTCCTCCAGG | TAATGATGAA | CCCTACACTG  | 60  |
| AGCAGATGGG | CAACTGTGGA | GAGAAGGGTG | AAAGGATCCA | CCTCACTCCT | GATTTTCATTG | 120 |
| CAGGAAAAAA | GTTAGCTGAA | TATGGACCAC | AAGGTAGGGC | ATTGTGCCAT | GAGTGGGCTC  | 180 |
| ATCTACGATG | GGGAGTATTT | GACGAGTACA | ATAATGATGA | GAAATTCTAC | TTATCCAATG  | 240 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CAAAAGATGC | ACATTCAATA | AAGTAACAGG | ACTCTATGAA | AAAGGATGTG | AGTTTGTTC  | 60  |
| CCAATCCCGC | CAGACGGAGA | AGGCTTCTAT | AATGTTTGCA | CAACATGTTG | ATTCTATAGT | 120 |
| TGAATTCTGT | ACAGAACAAA | ACCACAACAA | AGAAGCTCCA | AACAAGCAAA | ATCAAAAATG | 180 |
| C          |            |            |            |            |            | 181 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CTATAGTTGA | ATTCTGTACA | GAACAAAACC | ACAACAAAGA | AGCTCCAAAC | AAGCAAAATC | 60  |
| AAAAATGCAA | TCTCCGAAGC | ACATGGGAAG | TGATCCGTGA | TTCTGAGGAC | TTTAAGAAAA | 120 |
| CCACTCCTAT | GACAACACAG | CCACCAAATC | CCACCTTCTC | ATTGCTGCAG | ATTGGACAAA | 180 |
| GAATTGTGTG | TTTAGTCCTT | GACAAATCTG | GAAGCATGGC |            |            | 220 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CAAAGAATTG | TGTGTTTAGT | CCTTGACAAA | TCTGGAAGCA | TGGCGACTGG | TAACCGCCTC | 60  |
| AATCGACTGA | ATCAAGCAGG | CCAGCTTTTC | CTGCTGCAGA | CAGTTGAGCT | GGGTCCTGG  | 120 |
| GTTGGGATGG | TGACATTTGA | CAGTGCTGCC | CATGTACAAA | GTGAACTCAT | ACAGATAAAC | 180 |
| AGTGGCAGTG | ACAGGGACAC | ACTCGCCAAA | AGATTACCTG | CAGCAGCTTC | AGGAGGGACG | 240 |
| TCCATCTGCA | GC         |            |            |            |            | 252 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 92

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(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GAAATATCCA | ACTGATGGAT | CTGAAATTGT | GCTGCTGACG | GATGGGGAAG | ACAACACTAT | 60  |
| AAGTGGGTGC | TTTAACGAGG | TCAAACAAAG | TNGTGCCATC | ATCCACACAG | TCGCTTTGGG | 120 |
| GCCCTCTGCA | GCTCAAGAAC | TAGAGGAGCT | GTCCAAAATG | ACAGGAGGTT | TACAGACATA | 180 |
| TGCTTCAGAT | CAAGTTCAGA | ACAATGGCCT | CATTGATGCT | TTTGGGGCCC | TTTCATCAGG | 240 |
| AAATGGAGCT | GTCTCTCAGC | GCTCCATCCA | GCTTGAGAGT | AAGGGATTA  |            | 289 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| AACAAAGTGG | TGCCATCATC | CACACAGTCG | CTTTGGGGCC | CTCTGCAGCT | CAAGAACTAG | 60  |
| AGGAGCTGTC | CAAAATGACA | GGAGGTTTAC | AGACATATGC | TTCAGATCAA | GTTCAGAACA | 120 |
| ATGGCCTCAT | TGATGCTTTT | GGGGCCCTTT | CATCAGGAAA | TGGAGCTGTC | TCTCAGCGCT | 180 |
| CCATCCAGCT | TGAGAGTAAG | GGATTAACCC | TCCAGAACAG | CCAGTGGATG | AATGGCACAG | 240 |
| TGATCGTGGA | CAG        |            |            |            |            | 253 |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| GAACAATGGC | CTCATTGATG | CTTTTGGGGC | CCTTTTCATCA | GGAAATGGAG | CTGTCTCTCA | 60  |
| GCGCTCCATC | CAGCTTGAGA | GTAAGGGATT | AACCTTCCAG  | AACAGCCAGT | GGATGAATGG | 120 |
| CACAGTGATC | GTGGACAGCA | CCGTGGGAAA | GGACACTTTG  | TTTCTTATCA | CCTGGACAAC | 180 |
| GCAGCCTCCC | CAAATCCTTC | TCTGGGATCC | CAGTGGAC    |            |            | 218 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGCACAGTGA | TCGTGGACAG | CACCGTGGGA | AAGGACACTT | TGTTTCTTAT | CACCTGGACA | 60  |
| ACGCAGCCTC | CCCAAATCCT | TCTCTGGGAT | CCCAGTGGAC | AGAAGCAAGG | TGGCTTTGTA | 120 |
| GTGGACAAAA | ACACCAAAAT | GGCCTACCTC | CAAATCCCAG | GCATTGCTAA | GGTTGGCACT | 180 |
| TGGAAATACA | GTCTGCAAGC | AAGCTCACAA | ACCTTGACCC | TGACTGTCA  |            | 229 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GGCTTTGTAG | TGGACAAAAA | CACCAAAATG | GCCTACCTCC | AAATCCCAGG | CATTGCTAAG | 60  |
| GTTGGCACTT | GGAAATACAG | TCTGCAAGCA | AGCTCACAAA | CCTTGACCCT | GACTGTCACG | 120 |
| TCCCGTGCGT | CCAATGCTAC | CCTGCCTCCA | ATTACAGTGA | CTTCCAAAAC | GAACAAGGAC | 180 |
| ACCAGCAAAT | T          |            |            |            |            | 191 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GACACCAGCA | AATTCCCCAG | CCCTCTGGTA | GTTTATGCAA | ATATTCGCCA | AGGAGCCTCC | 60  |
| CCAATTCTCA | GGGCCAGTGT | CACAGCCCTG | ATTGAATCAG | TGAATGGAAA | AACAGTTACC | 120 |
| TTGGAACACT | TGGATAATGG | AGCAGGTGCT | GATGCTACTA | AGGATGACGG | TGTCTACTCA | 180 |
| AGGTATTTC  | CAACTTATGA | CACGAATGGT | AGATACAGTG | TAAAAGTGCG | GGCTC      | 235 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GTGCGGGCTC | TGGGAGGAGT | TAACGCAGCC | AGACGGAGAG | TGATACCCCA | GCAGAGTGGA | 60  |
| GCACTGTACA | TACCTGGCTG | GATTGAGAAT | GATGAAATAC | AATGGAATCC | ACCAAGACCT | 120 |
| GAAATTAATA | AGGATGATGT | TCAACACAAG | CAAGTGTGTT | TCAGCAGAAC | ATCCTCGGGA | 180 |
| GGCTCATTGT | TGGCTTCTGA | TGTCCCAAAT | GCTCCCATAC | CTGATCT    |            | 227 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ACCTGAAGGC | GGAAATTCAC | GGGGGCAGTC | TCATTAATCT | GACTTGGACA | GCTCCTGGGG | 60  |
| ATGATTATGA | CCATGGAACA | GCTCACAAGT | ATATCATTCG | AATAAGTACA | AGTATTCTTG | 120 |
| ATCTCAGAGA | CAAGTTCAAT | GAATCTCTTC | AAGTGAATAC | TACTGCTCTC | ATCCCAAAGG | 180 |
| AAGCCAACTC | TGAGGAAGTC | TTTTTGTTTA | AACCAGAAAA | CATTACTTTT | GAAAATGGCA | 240 |
| CAGATCTT   |            |            |            |            |            | 248 |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

58

862230 96964060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ACAGATCTTT | TCATTGCTAT | TCAGGCTGTT | GATAAGGTCG | ATCTGAAATC | AGAAATATCC | 60  |
| AACATTGCAC | GAGTATCTTT | GTTTATTCTT | CCACAGACTC | CGCCAGAGAC | ACCTAGTCCT | 120 |
| GATGAAACGT | CTGCTCCTTG | TCCTAATATT | CATA       |            |            | 154 |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GTTTATTCTT | CCACAGACTC | CGCCAGAGAC | ACCTAGTCCT | GATGAAACGT | CTGCTCCTTG | 60  |
| TCCTAATATT | CATATCAACA | GCACCATTC  | TGGCATTAC  | ATTTTAAAAA | TTATGTGGAA | 120 |
| GTGGATAGGA | GAAGTGCAGC | TGTCAATAGC | CTAGGGCTGA | ATTTTGTCA  | GATAAATAAA | 180 |
| ATAAATCATT | CATCCTTTTT | TTTGATTATA | AAATTTTCTA | AAATGTATTT | TAGACTTCCT | 240 |
| GT         |            |            |            |            |            | 242 |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| GGCATTACACA | TTTTAAAAAT | TATGTGGAAG | TGGATAGGAG | AACTGCAGCT | GTCAATAGCC | 60  |
| TAGGGCTGAA  | TTTTTGTCAG | ATAAATAAAA | TAAATCATTC | ATCCTT     |            | 106 |

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GAAATCACAG | GGAGATGTAC | AGCAATGGGG | CCATTTAAGA | GTTCTGTGTT | CATCTTGATT | 60  |
| CTTCACCTTC | TAGAAGGGGC | CCTGAGTAAT | TCACTCATTC | AGCTGAACAA | CAATGGCTAT | 120 |
| GAAGGCATTG | TCGTTGCAAT | CGACCCCAAT | GTGCCAGAAG | ATGAAACACT | CATTCAACAA | 180 |
| ATAAAGGACA | TGGTGACCCA | GGCATCTCTG | TATCTGTTTG | AAGCTACAGG | AAAGCGATTT | 240 |
| TATTTCAAAA | ATGTTGCCAT | TTTGATTCTT | GAAACATGGA | AGACAAAGGC | TGACTATGTG | 300 |
| AGACAAAAC  | TTGAGACCTA | CAAAAATGCT | GATGTTCTGG | TTGCTGAGTC | TACTCCTCCA | 360 |
| GGTAATGATG | AACCCTACAC | TGAGCAGATG | GGCAACTGTG | GAGAGAAGGG | TGAAAGGATC | 420 |
| CACCTCACTC | CTGATTTCAT | TGCAGGAAAA | AAGTTAGCTG | AATATGGACC | ACAAGGTAGG | 480 |
| GCATTTGTCC | ATGAGTGGGC | TCATCTACGA | TGGGGAGTAT | TTGACGAGTA | CAATAATGAT | 540 |
| GAGAAATTCT | ACTTATCCAA | TGGAAGAATA | CAAGCAGTAA | GATGTTTCAG | AGGTATTACT | 600 |
| GGTACAAATG | TAGTAAAGAA | GTGTCAGGGA | GGCAGCTGTT | ACACCAAAAG | ATGCACATTC | 660 |
| AATAAAGTAA | CAGGACTCTA | TGAAAAAGGA | TGTGAGTTTG | TTCTCCAATC | CCGCCAGACG | 720 |
| GAGAAGGCTT | CTATAATGTT | TGCACAACAT | GTTGATTCTA | TAGTTGAATT | CTGTACAGAA | 780 |
| CAAAACCACA | ACAAAGAAGC | TCCAAACAAG | CAAAATCAAA | AATGCAATCT | CCGAAGCACA | 840 |
| TGGGAAGTGA | TCCGTGATT  | TGAGGACTTT | AAGAAAACCA | CTCCTATGAC | AACACAGCCA | 900 |
| CCAAATCCCA | CCTTCTCATT | GCTGCAGATT | GGACAAAGAA | TTGTGTGTTT | AGTCCTTGAC | 960 |

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|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| AAATCTGGAA  | GCATGGCGAC | TGGTAACCGC | CTCAATCGAC  | TGAATCAAGC  | AGGCCAGCTT  | 1020 |
| TTCCTGCTGC  | AGACAGTTGA | GCTGGGGTCC | TGGGTTGGGA  | TGGTGACATT  | TGACAGTGCT  | 1080 |
| GCCCATGTAC  | AAAGTGAAC  | CATACAGATA | AACAGTGGCA  | GTGACAGGGA  | CACACTCGCC  | 1140 |
| AAAAGATTAC  | CTGCAGCAGC | TTCAGGAGGG | ACGTCCATCT  | GCAGCGGGCT  | TCGATCGGCA  | 1200 |
| TTTACTGTGA  | TTAGGAAGAA | ATATCCAAC  | GATGGATCTG  | AAATTGTGCT  | GCTGACGGAT  | 1260 |
| GGGGAAGACA  | ACACTATAAG | TGGGTGCTTT | AACGAGGTCA  | AACAAAGTGG  | TGCCATCATC  | 1320 |
| CACACAGTCG  | CTTTGGGGCC | CTCTGCAGCT | CAAGAACTAG  | AGGAGCTGTC  | CAAAATGACA  | 1380 |
| GGAGGTTTAC  | AGACATATGC | TTCAGATCAA | GTTTCAGAACA | ATGGCCTCAT  | TGATGCTTTT  | 1440 |
| GGGGCCCTTT  | CATCAGGAAA | TGGAGCTGTC | TCTCAGCGCT  | CCATCCAGCT  | TGAGAGTAAG  | 1500 |
| GGATTAACCC  | TCCAGAACAG | CCAGTGGATG | AATGGCACAG  | TGATCGTGGA  | CAGCACCGTG  | 1560 |
| GGAAAGGACA  | CTTTGTTTCT | TATCACCTGG | ACAACGCAGC  | CTCCCCAAAT  | CCTTCTCTGG  | 1620 |
| GATCCCAAGT  | GACAGAAGCA | AGGTGGCTTT | GATGTGGACA  | AAAAACACCA  | AATGGCCTAC  | 1680 |
| CTCCAAATCC  | CAGGCATTGC | TAAGGTGGC  | ACTTGGAAT   | ACAGTCTGCA  | AGCAAGCTCA  | 1740 |
| CAAACCTTGA  | CCCTGACTGT | CACGTCCCCT | GCGTCCAATG  | CTACCCTGCC  | TCCAATTACA  | 1800 |
| GTGACTTCCA  | AAACGAACAA | GGACACCAGC | AAATTCCCCA  | GCCCTCTGGT  | AGTTTATGCA  | 1860 |
| AATATTTCGCC | AAGGAGCCTC | CCCAATTCTC | AGGGCCAGTG  | TCACAGCCCT  | GATTGAATCA  | 1920 |
| GTGAATGGAA  | AAACAGTTAC | CTTGGAAC   | CTGGATAATG  | GAGCAGGTGC  | TGATGCTACT  | 1980 |
| AAGGATGACG  | GTGTCTACTC | AAGGTATTTT | ACAACCTATG  | ACACGAATGG  | TAGATACAGT  | 2040 |
| GTAAGAGTGC  | GGGCTCTGGG | AGGAGTTAAC | GCAGCCAGAC  | GGAGAGTGAT  | ACCCAGCAG   | 2100 |
| AGTGGAGCAC  | TGTACATACC | TGGCTGGATT | GAGAATGATG  | AAATACAATG  | GAATCCACCA  | 2160 |
| AGACCTGAAA  | TTAATAAGGA | TGATGTTCAA | CACAAGCAAG  | TGTGTTTCAG  | CAGAACATCC  | 2220 |
| TCGGGAGGCT  | CATTGTGGC  | TTCTGATGTC | CCAAATGCTC  | CCATACCTGA  | TCTCTTCCCA  | 2280 |
| CCTGGGCCAAA | TCACCGACCT | GAAGGCGGAA | ATTCACGGGG  | GCAGTCTCAT  | TAATCTGACT  | 2340 |
| TGGACAGCTC  | CTGGGGATGA | TTATGACCAT | GGAACAGCTC  | ACAAGTATAT  | CATTCTGAATA | 2400 |
| AGTACAAGTA  | TTCTTGATCT | CAGAGACAAG | TTCAATGAAT  | CTCTTCAAGT  | GAATACTACT  | 2460 |
| GCTCTCATCC  | CAAAGGAAGC | CAACTCTGAG | GAAGTCTTTT  | TGTTTAAACC  | AGAAAACATT  | 2520 |
| ACTTTTGAAA  | ATGGCACAGA | TCTTTTCATT | GCTATTTCAGG | CTGTTGATAA  | GGTCGATCTG  | 2580 |
| AAATCAGAAA  | TATCCAACAT | TGCACGAGTA | TCTTTGTTTA  | TTCTTCCACA  | GACTCCGCCA  | 2640 |
| GAGACACCTA  | GTCCTGATGA | AACGTCTGCT | CCTTGTCCTA  | ATATTTCATAT | CAACAGCACC  | 2700 |
| ATTCTTGGCA  | TTCACATTTT | AAAAATTATG | TGGAAGTGGA  | TAGGAGAACT  | GCAGCTGTCA  | 2760 |
| ATAGCCTAGG  | GCTGAATTTT | TGTCAGATAA | ATAAAATAAA  | TCATTTCATCC | TTA         | 2813 |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| AACAAAGTGG | TGCCATCATC  | CACACAGTCG  | CTTTGGGGCC | CTCTGCAGCT | CAAGAACTAG  | 60   |
| AGGAGCTGTC | CAAAATGACA  | GGAGGTTTAC  | AGACATATGC | TTCAGATCAA | GTTTCAGAACA | 120  |
| ATGGCCTTAC | TGATGCTTTT  | GGGGCCCTTT  | CATCAGGAAA | TGGAGCTGTC | TCTCAGCGCT  | 180  |
| CCATCCAGCT | TGAGAGTAAG  | GGATTAACCC  | TCCAGAACAG | CCAGTGGATG | AATGGCACAG  | 240  |
| TGATCGTGGA | CAGCACCGTG  | GGAAAGGACA  | CTTTGTTTCT | TATCACCTGG | ACAACGCAGC  | 300  |
| CTCCCCAAAT | CCTTCTCTGG  | GATCCCAGTG  | GACAGAAGCA | AGGTGGCTTT | GATGTGGACA  | 360  |
| AAAACACCAA | AATGGCCTAC  | CTCCAAATCC  | CAGGCATTGC | TAAGGTGGC  | ACTTGGAAT   | 420  |
| ACAGTCTGCA | AGCAAGCTCA  | CAAACCTTGA  | CCCTGACTGT | CACGTCCCCT | GCGTCCAATG  | 480  |
| CTACCCTGCC | TCCAATTACA  | GTGACTTCCA  | AAACGAACAA | GGACACCAGC | AAATTCCCCA  | 540  |
| GCCCTCTGGT | AGTTTATGCA  | AATATTTCGCC | AAGGAGCCTC | CCCAATTCTC | AGGGCCAGTG  | 600  |
| TCACAGCCCT | GATTGAATCA  | GTGAATGGAA  | AAACAGTTAC | CTTGGAAC   | CTGGATAATG  | 660  |
| GAGCAGGTGC | TGATGCTACT  | AAGGATGACG  | GTGTCTACTC | AAGGTATTTT | ACAACCTATG  | 720  |
| ACACGAATGG | TAGATACAGT  | GTAAGAGTGC  | GGGCTCTGGG | AGGAGTTAAC | GACGCCAGAC  | 780  |
| GGAGAGTGAT | ACCCAGCAG   | AGTGGAGCAC  | TGTACATACC | TGGCTGGATT | GAGAATGATG  | 840  |
| AAATACAATG | GAATCCACCA  | AGACCTGAAA  | TTAATAAGGA | TGATGTTCAA | CACAAGCAAG  | 900  |
| TGTGTTTCAG | CAGAACATCC  | TCGGGAGGCT  | CATTGTGGC  | TTCTGATGTC | CCAAATGCTC  | 960  |
| CCATACCTGA | TCTCTTCCCA  | CCTGGCCAAA  | TCACCGACCT | ATTCACGGGG |             | 1020 |
| GCAGTCTCAT | TAATCTGACT  | TGGACAGCTC  | CTGGGGATGA | TTATGACCAT | GGAACAGCTC  | 1080 |
| ACAAGTATAT | CATTCTGAATA | AGTACAAGTA  | TTCTTGATCT | CAGAGACAAG | TTCAATGAAT  | 1140 |
| CTCTTCAAGT | GAATACTACT  | GCTCTCATCC  | CAAAGGAAGC | CAACTCTGAG | GAAGTCTTTT  | 1200 |
| TGTTTAAACC | AGAAAACATT  | ACTTTTGAAA  | ATGGCAGAGA | TCTTTTCATT | GCTATTTCAGG | 1260 |
| CTGTTGATAA | GGTCGATCTG  | AAATCAGAAA  | TATCCAACAT | TGCACGAGTA | TCTTTGTTTA  | 1320 |
| TTCTTCCACA | GACTCCGCCA  | GAGACACCTA  | GTCCTGATGA | AACGTCTGCT | CCTTGTCCTA  | 1380 |

|            |            |            |            |            |             |      |
|------------|------------|------------|------------|------------|-------------|------|
| ATATTCATAT | CAACAGCACC | ATTCCTGGCA | TTCACATTTT | AAAAATTATG | TGGAAGTGGA  | 1440 |
| TAGGAGAACT | GCAGCTGTCA | ATAGCCTAGG | GCTGAATTTT | TGTCAGATAA | ATAAAATAAA  | 1500 |
| TCATTCATCC | TTTTTTTTGA | TTATAAAATT | TTCTAAAATG | TATTTTAGAC | TTCCTGTAGG  | 1560 |
| GGCGATATA  | CTAAATGTAT | ATAGTACATT | TATACTAAAT | GTATTCCTGT | AGGGGGCGAT  | 1620 |
| ATACTAAATG | TATTTTAGAC | TTCCTGTAGG | GGGCGATAAA | ATAAAATGCT | AAACAACCTGG | 1680 |
| GTA        |            |            |            |            |             | 1683 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2983 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| GAAATCACAG | GGAGATGTAC | AGCAATGGGG  | CCATTTAAGA  | GTTCTGTGTT  | CATCTTGATT  | 60   |
| CTTCACCTTC | TAGAAGGGGC | CCTGAGTAAT  | TCACTCATT   | AGCTGAACAA  | CAATGGCTAT  | 120  |
| GAAGGCATTG | TCGTTCGAAT | CGACCCCAAT  | GTGCCAGAAG  | ATGAAACACT  | CATTCAACAA  | 180  |
| ATAAAGGACA | TGGTGACCCA | GGCATCTCTG  | TATCTGTTTG  | AAGCTACAGG  | AAAGCGATT   | 240  |
| TATTTCAAAA | ATGTTGCCAT | TTTGATTCCCT | GAAACATGGA  | AGACAAAGGC  | TGACTATGTG  | 300  |
| AGACCAAAAC | TTGAGACCTA | CAAAAATGCT  | GATGTTCTGG  | TTGCTGAGTC  | TACTCCTCCA  | 360  |
| GGTAATGATG | AACCCTACAC | TGAGCAGATG  | GGCAACTGTG  | GAGAGAAGGG  | TGAAAGGATC  | 420  |
| CACCTCACTC | CTGATTTCAT | TGCAGGAAAA  | AAGTTAGCTG  | AATATGGACC  | ACAAGGTAGG  | 480  |
| GCATTTGTCC | ATGAGTGGGC | TCATCTACGA  | TGGGGAGTAT  | TTGACGAGTA  | CAATAATGAT  | 540  |
| GAGAAATTCT | ACTTATCCAA | TGGAAGAATA  | CAAGCAGTAA  | GATGTTTCAG  | AGGTATTACT  | 600  |
| GGTACAAATG | TAGTAAAGAA | GTGTCAGGGA  | GGCAGCTGTT  | ACACCAAAAAG | ATGCACATTC  | 660  |
| AATAAAGTAA | CAGGACTCTA | TGAAAAAGGA  | TGTGAGTTTG  | TTCTCCAATC  | CCGCCAGACG  | 720  |
| GAGAAGGCTT | CTATAATGTT | TGCACAACAT  | GTTGATTCTA  | TAGTTGAATT  | CTGTACAGAA  | 780  |
| CAAAACCACA | CAAAGGAAGC | TCCAACAACG  | CAAAATCAAA  | AATGCAATCT  | CCGAAGCACA  | 840  |
| TGGGAAGTGA | TCCGTGATT  | TGAGGACTTT  | AAGAAAACCA  | CTCCTATGAC  | AACACAGCCA  | 900  |
| CCAAATCCCA | CCTTCTCATT | GCTGCAGATT  | GGACAAAGAA  | TTGTGTGTTT  | AGTCCTTGAC  | 960  |
| AAATCTGGAA | GCATGGCGAC | TGGTAACCGC  | CTCAATCGAC  | TGAATCAAGC  | AGGCCAGCTT  | 1020 |
| TTCTCTGCTG | AGACAGTTGA | GCTGGGGTCC  | TGGGTTGGGA  | TGGTGACATT  | TGACAGTGCT  | 1080 |
| GCCCATGTAC | AAAGTGAAC  | CATACAGATA  | AACAGTGGCA  | GTGACAGGGA  | CACACTCGCC  | 1140 |
| AAAAGATTAC | CTGCAGCAGC | TTCAGGAGGG  | ACGTCCATCT  | GCAGCGGGCT  | TCGATCGGCA  | 1200 |
| TTTACTGTGA | TTAGGAAGAA | ATATCCAAC   | GATGGATCTG  | AAATTGTGCT  | GCTGACGGAT  | 1260 |
| GGGGAAGACA | ACACTATAAG | TGGGTGCTTT  | AACGAGGTCA  | AACAAAGTGG  | TGCCATCATC  | 1320 |
| CACACAGTCG | CTTTGGGGCC | CTCTGCAGCT  | CAAGAAGTAG  | AGGAGCTGTC  | CAAAATGACA  | 1380 |
| GGAGGTTTAC | AGACATATGC | TTCAGATCAA  | GTTTCAGAAC  | ATGGCCTCAT  | TGATGCTTTT  | 1440 |
| GGGGCCCTTT | CATCAGGAAA | TGGAGCTGTC  | TCTCAGCGCT  | CCATCCAGCT  | TGAGAGTAAG  | 1500 |
| GGATTAACCC | TCCAGAACAG | CCAGTGGATG  | AATGGCACAG  | TGATCGTGGA  | CAGCACCGTG  | 1560 |
| GGAAAGGACA | CTTTGTTTCT | TATCACCTGG  | ACAACGCAGC  | CTCCCCAAAT  | CCTTCTCTGG  | 1620 |
| GATCCCAGTG | GACAGAAGCA | AGGTGGCTTT  | GTAGTTGGACA | AAAACACCAA  | AATGGCCTAC  | 1680 |
| CTCCAAATCC | CAGGCATTGC | TAAGGTTGGC  | ACTTGGAAT   | ACAGTCTGCA  | AGCAAGCTCA  | 1740 |
| CAAACCTTGA | CCCTGACTGT | CACGTCCCCT  | GCGTCCAATG  | CTACCCCTGCC | TCCAATTACA  | 1800 |
| GTGACTTCCA | AAACGAACAA | GGACACCAGC  | AAATTCCTCCA | GCCCTCTGGT  | AGTTTATGCA  | 1860 |
| AATATTGCGC | AAGGAGCCTC | CCCAATTCTC  | AGGGCCAGTG  | TCACAGCCCT  | GATTGAATCA  | 1920 |
| GTGAATGGAA | AAACAGTTAC | CTTGGAAC    | CTGGATAATG  | GAGCAGGTGC  | TGATGCTACT  | 1980 |
| AAGGATGACG | GTGTCTACTC | AAGGTATTTT  | ACAACCTTATG | ACACGAATGG  | TAGATACAGT  | 2040 |
| GTAAAAGTGC | GGGCTCTGGG | AGGAGTTAAT  | GCAGCCAGAC  | GGAGAGTGAT  | ACCCAGCAG   | 2100 |
| AGTGAGGAC  | TGTACATACC | TGGCTGGATT  | GAGAATGATG  | AAATACAATG  | GAATCCACCA  | 2160 |
| AGACCTGAAA | TTAATAAGGA | TGATGTTCAA  | CACAAGCAAG  | TGTGTTTCAG  | CAGAACATCC  | 2220 |
| TCGGGAGGCT | CATTTGTGGC | TTCTGATGTC  | CCAAATGCTC  | CCATACCTGA  | TCTCTTCCCA  | 2280 |
| CCTGGCCAAA | TCACCGACCT | GAAGGCGGAA  | ATTCACGGGG  | GCAGTCTCAT  | TAATCTGACT  | 2340 |
| TGGACAGCTC | CTGGGGATGA | TTATGACCAT  | GGAACAGCTC  | ACAAGTATAT  | CATTCTGAATA | 2400 |
| AGTACAAGTA | TTCTTGATCT | CAGAGACAAG  | TTCAATGAAT  | CTCTTCAAGT  | GAATACTACT  | 2460 |
| GCTCTCATCC | CAAAGGAAGC | CAACTCTGAG  | GAAGTCTTTT  | TGTTTAAACC  | AGAAAACATT  | 2520 |
| ACTTTTGAAA | ATGGCACAGA | TCTTTTCATT  | GCTATTTCAGG | CTGTTGATAA  | GGTCGATCTG  | 2580 |
| AAATCAGAAA | TATCCAACAT | TGCACGAGTA  | TCTTTGTTTA  | TTCTCCACA   | GACTCCGCCA  | 2640 |
| GAGACACCTA | GTCCTGATGA | AACGTCTGCT  | CCTTGTCTTA  | ATATTCATAT  | CAACAGCACC  | 2700 |
| ATTCCTGGCA | TTCACATTTT | AAAAATTATG  | TGGAAGTGGG  | TAGGAGAACT  | GCAGCTGTCA  | 2760 |
| ATAGCCTAGG | CTGAATTTT  | TGTCAGATAA  | ATAAAATAAA  | TCATTCATCC  | TTTTTTTTGA  | 2820 |
| TTATAAAATT | TTCTAAAATG | TATTTTAGAC  | TTCCTGTAGG  | GGGCGATATA  | CTAAATGTAT  | 2880 |

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ATAGTACATT TATACTAAAT GTATTCCTGT AGGGGGCGAT ATACTAAATG TATTTTAGAC 2940  
TTCCTGTAGG GGGCGATAAA ATAAAATGCT AAACAACCTGG GTA 2983

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC 60  
CGGGAATT 68

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG 60  
GAATTCCG 68

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCGGATAAC AATTTACAC AGGA 24

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGTAAAACGA CGGCCAGT 18

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAAGCAAGGT GGCTTTGTAG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAGCTCACAA ACCTTGACCC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TACAGTGTA AAGTGCGGGC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTGGGGATG ATTATGACCA

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACGTCTGCTC CTTGTCCTAA

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

93

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GCAGACGTTT CATCAGGACT

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGGGAAGAGA TCAGGTATGG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGAGCCCGC ACTTTTACAC

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACAGTCAGGG TCAAGGTTTG

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTGGAGGGTT AATCCCTTAC

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCCTATGACA ACACAGCCAC

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GATGTTCTGG TTGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGCTGTGTTG TCATAGGAGT G

21

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGTTCATCAT TACCTGGAGG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCCACCTCAC TCCTGATTTC ATTGC

25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TGATTCAGTC GATTGAGGCG GTTAC

25

95

05049696.032798

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Pro | Phe | Lys | Ser | Ser | Val | Phe | Ile | Leu | Ile | Leu | His | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Gly | Ala | Leu | Ser | Asn | Ser | Leu | Ile | Gln | Leu | Asn | Asn | Asn | Gly | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Ile | Val | Val | Ala | Ile | Asp | Pro | Asn | Val | Pro | Glu | Asp | Glu | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ile | Gln | Gln | Ile | Lys | Asp | Met | Val | Thr | Gln | Ala | Ser | Leu | Tyr | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Glu | Ala | Thr | Gly | Lys | Arg | Phe | Tyr | Phe | Lys | Asn | Val | Ala | Ile | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Pro | Glu | Thr | Trp | Lys | Thr | Lys | Ala | Asp | Tyr | Val | Arg | Pro | Lys | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Thr | Tyr | Lys | Asn | Ala | Asp | Val | Leu | Val | Ala | Glu | Ser | Thr | Pro | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Asn | Asp | Glu | Pro | Tyr | Thr | Glu | Gln | Met | Gly | Asn | Cys | Gly | Glu | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Glu | Arg | Ile | His | Leu | Thr | Pro | Asp | Phe | Ile | Ala | Gly | Lys | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Glu | Tyr | Gly | Pro | Gln | Gly | Arg | Ala | Phe | Val | His | Glu | Trp | Ala | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Arg | Trp | Gly | Val | Phe | Asp | Glu | Tyr | Asn | Asn | Asp | Glu | Lys | Phe | Tyr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ser | Asn | Gly | Arg | Ile | Gln | Ala | Val | Arg | Cys | Ser | Ala | Gly | Ile | Thr |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Thr | Asn | Val | Val | Lys | Lys | Cys | Gln | Gly | Gly | Ser | Cys | Tyr | Thr | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Cys | Thr | Phe | Asn | Lys | Val | Thr | Gly | Leu | Tyr | Glu | Lys | Gly | Cys | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Val | Leu | Gln | Ser | Arg | Gln | Thr | Glu | Lys | Ala | Ser | Ile | Met | Phe | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | His | Val | Asp | Ser | Ile | Val | Glu | Phe | Cys | Thr | Glu | Gln | Asn | His | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Glu | Ala | Pro | Asn | Lys | Gln | Asn | Gln | Lys | Cys | Asn | Leu | Arg | Ser | Thr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Trp | Glu | Val | Ile | Arg | Asp | Ser | Glu | Asp | Phe | Lys | Lys | Thr | Thr | Pro | Met |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Thr | Thr | Gln | Pro | Pro | Asn | Pro | Thr | Phe | Ser | Leu | Leu | Gln | Ile | Gly | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Arg | Ile | Val | Cys | Leu | Val | Leu | Asp | Lys | Ser | Gly | Ser | Met | Ala | Thr | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Arg | Leu | Asn | Arg | Leu | Asn | Gln | Ala | Gly | Gln | Leu | Phe | Leu | Leu | Gln |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Thr | Val | Glu | Leu | Gly | Ser | Trp | Val | Gly | Met | Val | Thr | Phe | Asp | Ser | Ala |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | His | Val | Gln | Ser | Glu | Leu | Ile | Gln | Ile | Asn | Ser | Gly | Ser | Asp | Arg |
|     | 355 |     |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Asp | Thr | Leu | Ala | Lys | Arg | Leu | Pro | Ala | Ala | Ala | Ser | Gly | Gly | Thr | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ile | Cys | Ser | Gly | Leu | Arg | Ser | Ala | Phe | Thr | Val | Ile | Arg | Lys | Lys | Tyr |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Pro | Thr | Asp | Gly | Ser | Glu | Ile | Val | Leu | Leu | Thr | Asp | Gly | Glu | Asp | Asn |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Thr | Ile | Ser | Gly | Cys | Phe | Asn | Glu | Val | Lys | Gln | Ser | Gly | Ala | Ile | Ile |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| His | Thr | Val | Ala | Leu | Gly | Pro | Ser | Ala | Ala | Gln | Glu | Leu | Glu | Glu | Leu |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |
| Ser | Lys | Met | Thr | Gly | Gly | Leu | Gln | Thr | Tyr | Ala | Ser | Asp | Gln | Val | Gln |  |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |
| Asn | Asn | Gly | Leu | Ile | Asp | Ala | Phe | Gly | Ala | Leu | Ser | Ser | Gly | Asn | Gly |  |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |  |
| Ala | Val | Ser | Gln | Arg | Ser | Ile | Gln | Leu | Glu | Ser | Lys | Gly | Leu | Thr | Leu |  |  |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     |     | 495 |  |  |
| Gln | Asn | Ser | Gln | Trp | Met | Asn | Gly | Thr | Val | Ile | Val | Asp | Ser | Thr | Val |  |  |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |  |
| Gly | Lys | Asp | Thr | Leu | Phe | Leu | Ile | Thr | Trp | Thr | Thr | Gln | Pro | Pro | Gln |  |  |
|     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |  |
| Ile | Leu | Leu | Trp | Asp | Pro | Ser | Gly | Gln | Lys | Gln | Gly | Gly | Phe | Val | Val |  |  |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |  |
| Asp | Lys | Asn | Thr | Lys | Met | Ala | Tyr | Leu | Gln | Ile | Pro | Gly | Ile | Ala | Lys |  |  |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |  |
| Val | Gly | Thr | Trp | Lys | Tyr | Ser | Leu | Gln | Ala | Ser | Ser | Gln | Thr | Leu | Thr |  |  |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |  |
| Leu | Thr | Val | Thr | Ser | Arg | Ala | Ser | Asn | Ala | Thr | Leu | Pro | Pro | Ile | Thr |  |  |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |  |  |
| Val | Thr | Ser | Lys | Thr | Asn | Lys | Asp | Thr | Ser | Lys | Phe | Pro | Ser | Pro | Leu |  |  |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |  |  |
| Val | Val | Tyr | Ala | Asn | Ile | Arg | Gln | Gly | Ala | Ser | Pro | Ile | Leu | Arg | Ala |  |  |
|     | 610 |     |     |     | 615 |     |     |     |     |     | 620 |     |     |     |     |  |  |
| Ser | Val | Thr | Ala | Leu | Ile | Glu | Ser | Val | Asn | Gly | Lys | Thr | Val | Thr | Leu |  |  |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |  |  |
| Glu | Leu | Leu | Asp | Asn | Gly | Ala | Gly | Ala | Asp | Ala | Thr | Lys | Asp | Asp | Gly |  |  |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |  |  |
| Val | Tyr | Ser | Arg | Tyr | Phe | Thr | Thr | Tyr | Asp | Thr | Asn | Gly | Arg | Tyr | Ser |  |  |
|     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |  |  |
| Val | Lys | Val | Arg | Ala | Leu | Gly | Gly | Val | Asn | Ala | Ala | Arg | Arg | Arg | Val |  |  |
|     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |  |  |
| Ile | Pro | Gln | Gln | Ser | Gly | Ala | Leu | Tyr | Ile | Pro | Gly | Trp | Ile | Glu | Asn |  |  |
|     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |     |  |  |
| Asp | Glu | Ile | Gln | Trp | Asn | Pro | Pro | Arg | Pro | Glu | Ile | Asn | Lys | Asp | Asp |  |  |
| 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |  |  |
| Val | Gln | His | Lys | Gln | Val | Cys | Phe | Ser | Arg | Thr | Ser | Ser | Gly | Gly | Ser |  |  |
|     |     |     |     | 725 |     |     |     |     | 730 |     |     |     |     | 735 |     |  |  |
| Phe | Val | Ala | Ser | Asp | Val | Pro | Asn | Ala | Pro | Ile | Pro | Asp | Leu | Phe | Pro |  |  |
|     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |  |  |
| Pro | Gly | Gln | Ile | Thr | Asp | Leu | Lys | Ala | Glu | Ile | His | Gly | Gly | Ser | Leu |  |  |
|     |     |     | 755 |     |     |     | 760 |     |     |     |     | 765 |     |     |     |  |  |
| Ile | Asn | Leu | Thr | Trp | Thr | Ala | Pro | Gly | Asp | Asp | Tyr | Asp | His | Gly | Thr |  |  |
|     | 770 |     |     |     |     | 775 |     |     |     |     | 780 |     |     |     |     |  |  |
| Ala | His | Lys | Tyr | Ile | Ile | Arg | Ile | Ser | Thr | Ser | Ile | Leu | Asp | Leu | Arg |  |  |
| 785 |     |     |     |     | 790 |     |     |     |     | 795 |     |     |     |     | 800 |  |  |
| Asp | Lys | Phe | Asn | Glu | Ser | Leu | Gln | Val | Asn | Thr | Thr | Ala | Leu | Ile | Pro |  |  |
|     |     |     |     | 805 |     |     |     |     | 810 |     |     |     |     | 815 |     |  |  |
| Lys | Glu | Ala | Asn | Ser | Glu | Glu | Val | Phe | Leu | Phe | Lys | Pro | Glu | Asn | Ile |  |  |
|     |     |     | 820 |     |     |     |     | 825 |     |     |     |     | 830 |     |     |  |  |
| Thr | Phe | Glu | Asn | Gly | Thr | Asp | Leu | Phe | Ile | Ala | Ile | Gln | Ala | Val | Asp |  |  |
|     |     |     | 835 |     |     |     | 840 |     |     |     |     | 845 |     |     |     |  |  |
| Lys | Val | Asp | Leu | Lys | Ser | Glu | Ile | Ser | Asn | Ile | Ala | Arg | Val | Ser | Leu |  |  |
|     | 850 |     |     |     |     | 855 |     |     |     |     | 860 |     |     |     |     |  |  |
| Phe | Ile | Pro | Pro | Gln | Thr | Pro | Pro | Glu | Thr | Pro | Ser | Pro | Asp | Glu | Thr |  |  |
| 865 |     |     |     |     | 870 |     |     |     |     | 875 |     |     |     |     | 880 |  |  |
| Ser | Ala | Pro | Cys | Pro | Asn | Ile | His | Ile | Asn | Ser | Thr | Ile | Pro | Gly | Ile |  |  |
|     |     |     |     | 885 |     |     |     |     | 890 |     |     |     |     | 895 |     |  |  |
| His | Ile | Leu | Lys | Ile | Met | Trp | Lys | Trp | Ile | Gly | Glu | Leu | Gln | Leu | Ser |  |  |
|     |     |     | 900 |     |     |     |     | 905 |     |     |     |     | 910 |     |     |  |  |
| Ile | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:42:

97

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Tyr Asn Asn Asp Glu Lys Phe Tyr Leu Ser Asn Gly Arg Ile Gln Ala  
 1 5 10 15  
 Val Arg Cys

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Tyr Thr Lys Arg Cys Thr Phe Asn Lys Val Thr Gly Leu Tyr Glu Lys  
 1 5 10 15  
 Gly Cys Glu Phe Val Leu Gln Ser  
 20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asn Ser Gly Ser Asp Arg Asp Thr Leu Ala Lys Arg Leu Pro Ala Ala  
 1 5 10 15  
 Ala Ser Gly Gly  
 20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Thr Trp Thr Thr Gln Pro Pro Gln Ile Leu Leu Trp Asp Pro Ser Gly  
 1 5 10 15  
 Gln Lys Gln Gly Phe Val Val Asp Lys Asn Thr Lys  
 20 25

98

03049696.032998

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ile Thr Val Thr Ser Lys Thr Asn Lys Asp Thr Ser Lys Phe Pro Ser  
1 5 10 15  
Pro Leu Val Val Tyr Ala Asn Ile Arg Gln Gly Ala Ser  
20 25

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asp Asn Gly Ala Gly Ala Asp Ala Thr Lys Asp Asp Gly Val Tyr Ser  
1 5 10 15  
Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser Val Lys  
20 25 30

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Trp Ile Glu Asn Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile  
1 5 10 15  
Asn Lys Asp Asp Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser  
20 25 30  
Ser Gly Gly  
35

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

99

09049696-032799



Glu Ile Asn Lys Asp Asp Val Gln His Lys Gln Val Cys Phe Ser Arg  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His  
1 5 10 15  
His His His His His  
20

00045696-032798